



21.US18.CIP.revised.ST25  
SEQUENCE LISTING

<110> Chen, Ruoping  
Chu, Zhi Liang  
Dang, Huong T.  
Lowitz, Kevin P.  
Pride, Cameron

<120> Endogenous and Non-Endogenous Versions of Human G Protein-Coupled  
Receptors

<130> 21.US18.CIP

<140> 09/995,225  
<141> 2001-11-26

<150> 09/170,496  
<151> 1998-10-13

<150> PCT/US99/23938  
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<150> 60/253,404  
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<170> PatentIn version 3.2

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Gly Leu Val Val Gly Val Pro Val Gly Leu Cys Tyr Asn Ala Leu Leu
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Val Leu Ala Asn Leu His Ser Lys Ala Ser Met Thr Met Pro Asp Val
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Tyr Phe Val Asn Met Ala Val Ala Gly Leu Val Leu Ser Ala Leu Ala  
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 Pro Val His Leu Leu Gly Pro Pro Ser Ser Arg Trp Ala Leu Trp Ser  
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 Val Gly Gly Glu Val His Val Ala Leu Gln Ile Pro Phe Asn Val Ser  
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 Ser Leu Val Ala Met Tyr Ser Thr Ala Leu Leu Ser Leu Asp His Tyr  
 115 120 125  
 Ile Glu Arg Ala Leu Pro Arg Thr Tyr Met Ala Ser Val Tyr Asn Thr  
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 Arg His Val Cys Gly Phe Val Trp Gly Gly Ala Leu Leu Thr Ser Phe  
 145 150 155 160  
 Ser Ser Leu Leu Phe Tyr Ile Cys Ser His Val Ser Thr Arg Ala Leu  
 165 170 175  
 Glu Cys Ala Lys Met Gln Asn Ala Glu Ala Ala Asp Ala Thr Leu Val  
 180 185 190  
 Phe Ile Gly Tyr Val Val Pro Ala Leu Ala Thr Leu Tyr Ala Leu Val  
 195 200 205  
 Leu Leu Ser Arg Val Arg Arg Glu Asp Thr Pro Leu Asp Arg Asp Thr  
 210 215 220  
 Gly Arg Leu Glu Pro Ser Ala His Arg Leu Leu Val Ala Thr Val Cys  
 225 230 235 240  
 Thr Gln Phe Gly Leu Trp Thr Pro His Tyr Leu Ile Leu Leu Gly His  
 245 250 255  
 Thr Val Ile Ile Ser Arg Gly Lys Pro Val Asp Ala His Tyr Leu Gly  
 260 265 270  
 Leu Leu His Phe Val Lys Asp Phe Ser Lys Leu Leu Ala Phe Ser Ser  
 275 280 285  
 Ser Phe Val Thr Pro Leu Leu Tyr Arg Tyr Met Asn Gln Ser Phe Pro  
 290 295 300  
 Ser Lys Leu Gln Arg Leu Met Lys Lys Leu Pro Cys Gly Asp Arg His  
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Val Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg  
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Ser Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val  
50 55 60

Phe Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr  
65 70 75 80

Trp Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His  
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Ile His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr  
100 105 110

Arg Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg  
115 120 125

Lys Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile  
130 135 140

Val Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu  
145 150 155 160

Tyr Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr  
165 170 175

Tyr Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val  
180 185 190

Ala Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val  
195 200 205

Gln Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln  
210 215 220

Leu Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro  
225 230 235 240

Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn  
245 250 255

Ala Cys Asn Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val  
260 265 270

Thr Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser  
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Gly Gln Pro Arg Val Thr Leu Leu Pro Thr Pro Asn Val Ser Gly Leu  
35 40 45

Ser Gln Glu Phe Glu Ser His Trp Pro Glu Ile Ala Glu Arg Ser Pro  
50 55 60

Cys Val Ala Gly Val Ile Pro Val Ile Tyr Tyr Ser Val Leu Leu Gly  
65 70 75 80

Leu Gly Leu Pro Val Ser Leu Leu Thr Ala Val Ala Leu Ala Arg Leu  
85 90 95

Ala Thr Arg Thr Arg Arg Pro Ser Tyr Tyr Tyr Leu Leu Ala Leu Thr  
100 105 110

Ala Ser Asp Ile Ile Ile Gln Val Val Ile Val Phe Ala Gly Phe Leu  
115 120 125

Leu Gln Gly Ala Val Leu Ala Arg Gln Val Pro Gln Ala Val Val Arg  
130 135 140

Thr Ala Asn Ile Leu Glu Phe Ala Ala Asn His Ala Ser Val Trp Ile  
145 150 155 160

Ala Ile Leu Leu Thr Val Asp Arg Tyr Thr Ala Leu Cys His Pro Leu  
165 170 175

His His Arg Ala Ala Ser Ser Pro Gly Arg Thr Arg Arg Ala Ile Ala  
180 185 190

Ala Val Leu Ser Ala Ala Leu Leu Thr Gly Ile Pro Phe Tyr Trp Trp  
195 200 205

Leu Asp Met Trp Arg Asp Thr Asp Ser Pro Arg Thr Leu Asp Glu Val  
210 215 220

Leu Lys Trp Ala His Cys Leu Thr Val Tyr Phe Ile Pro Cys Gly Val  
225 230 235 240

Phe Leu Val Thr Asn Ser Ala Ile Ile His Arg Leu Arg Arg Arg Gly  
245 250 255

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Arg Ser Gly Leu Gln Pro Arg Val Gly Lys Ser Thr Ala Ile Leu Leu  
260 265 270

Gly Ile Thr Thr Leu Phe Thr Leu Leu Trp Ala Pro Arg Val Phe Val  
275 280 285

Met Leu Tyr His Met Tyr Val Ala Pro Val His Arg Asp Trp Arg Val  
290 295 300

His Leu Ala Leu Asp Val Ala Asn Met Val Ala Met Leu His Thr Ala  
305 310 315 320

Ala Asn Phe Gly Leu Tyr Cys Phe Val Ser Lys Thr Phe Arg Ala Thr  
325 330 335

Val Arg Gln Val Ile His Asp Ala Tyr Leu Pro Cys Thr Leu Ala Ser  
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35 40 45

Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu  
50 55 60

Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn  
65 70 75 80

Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu  
85 90 95

Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His  
100 105 110

Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr  
115 120 125

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln  
130 135 140

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Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala  
145 150 155 160

Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe  
165 170 175

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser  
180 185 190

Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp  
195 200 205

Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val  
210 215 220

Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg  
225 230 235 240

Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser  
245 250 255

Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser  
260 265 270

Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu  
275 280 285

Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe  
290 295 300

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu  
305 310 315 320

Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys  
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Met Ser Ser Asn Ser Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala
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Asn Val Asn Gly Ser Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg
20           25           30

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Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe
35           40           45

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Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His

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55

60

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 Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser  
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 Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp  
 100 105 110  
 Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile  
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 Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe  
 130 135 140  
 Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro  
 145 150 155 160  
 Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Tyr Asp Asp Gly  
 165 170 175  
 Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile Gly Gly Cys Gln Thr  
 180 185 190  
 Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe Leu Ser Phe Phe Ile  
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 Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn Ile Phe Leu Val Ala  
 210 215 220  
 Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Gly Ser Lys Thr Glu Ser  
 225 230 235 240  
 Ser Ser Glu Ser Tyr Lys Ala Arg Val Ala Arg Arg Glu Arg Lys Ala  
 245 250 255  
 Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile Ser Trp Leu  
 260 265 270  
 Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly Phe Ile Thr  
 275 280 285  
 Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr Tyr Asn Ser  
 290 295 300

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Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys  
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Ala Ile Lys Val Ile Val Thr Gly Gln Val Leu Lys Asn Ser Ser Ala  
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Thr Met Asn Leu Phe Ser Glu His Ile  
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<213> Artificial

<220>  
<223> Novel Sequence

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<400> 12

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Met Met Pro Phe Cys His Asn Ile Ile Asn Ile Ser Cys Val Lys Asn
1      5      10      15

Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu
20      25      30

Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile
35      40      45

Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser
50      55      60

Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser
65      70      75      80

Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys
85      90      95

Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe
100     105     110

His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro
115     120     125

Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile
130     135     140

Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe
145     150     155     160

Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val
165     170     175

His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val
180     185     190

Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys
195     200     205

Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile
210     215     220

Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly
225     230     235     240

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Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val  
245 250 255

Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val  
260 265 270

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val  
275 280 285

Leu Ile Trp Phe Gly Tyr Leu Asn Ser Thr Phe Asn Pro Met Val Tyr  
290 295 300

Ala Phe Phe Tyr Pro Trp Phe Arg Lys Ala Leu Lys Met Met Leu Phe  
305 310 315 320

Gly Lys Ile Phe Gln Lys Asp Ser Ser Arg Cys Lys Leu Phe Leu Glu  
325 330 335

Leu Ser Ser

<210> 13  
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<220>  
<223> Novel Sequence

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gggtctttgc tggctgtatt tggaaatctc ttagtaatga cttctgttct tcattttaag 180  
cagctgcact ctccaaccaa ttttctcatt gcctctctgg cctgtgctga cttcttggtg 240  
ggtgtgactg tgatgctttt cagcatggtc aggacgggtg agagctgctg gtattttgga 300  
gccaaatttt gtactcttca cagttgctgt gatgtggcat tttgttactc ttctgtcctc 360  
cacttgctgt tcactctgcat cgacaggtac attgtgggta ctgatcccct ggtctatgct 420  
accaagttca ccgtgtctgt gtcgggaatt tgcacagcg tgccttgat tctgcctctc 480  
acgtacacgc gtgctgtgtt ctacacaggt gtcaatgatg atgggctgga ggaattagta 540  
agtgtcttca actgctgtagg tggctgtcaa attattgtaa gtcaaggctg ggtgttgata 600  
gattttctgt tattcttcat acctaccctt gttatgataa ttctttacag taagattttt 660  
cttatagcta aacaacaagc tataaaaatt gaaactacta gtagcaaagt agaatcatcc 720  
tcagagagtt ataaaatcag agtggccaag agagagagga aagcagctaa aaccctgggg 780

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gtcacggtac tagcatttgt tatttcatgg ttaccgtata cagttgatat attaattgat 840  
gcctttatgg gcttcctgac ccctgcctat atctatgaaa tttgctgttg gagtgcttat 900  
tataactcag ccatgaatcc tttgatttat gctctatttt atccttggtt taggaaagcc 960  
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ttagaataa 1029

<210> 14  
<211> 342  
<212> PRT  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 14

Met Thr Ser Asn Phe Ser Gln Pro Val Val Gln Leu Cys Tyr Glu Asp  
1 5 10 15

Val Asn Gly Ser Cys Ile Glu Thr Pro Tyr Ser Pro Gly Ser Arg Val  
20 25 30

Ile Leu Tyr Thr Ala Phe Ser Phe Gly Ser Leu Leu Ala Val Phe Gly  
35 40 45

Asn Leu Leu Val Met Thr Ser Val Leu His Phe Lys Gln Leu His Ser  
50 55 60

Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala Cys Ala Asp Phe Leu Val  
65 70 75 80

Gly Val Thr Val Met Leu Phe Ser Met Val Arg Thr Val Glu Ser Cys  
85 90 95

Trp Tyr Phe Gly Ala Lys Phe Cys Thr Leu His Ser Cys Cys Asp Val  
100 105 110

Ala Phe Cys Tyr Ser Ser Val Leu His Leu Cys Phe Ile Cys Ile Asp  
115 120 125

Arg Tyr Ile Val Val Thr Asp Pro Leu Val Tyr Ala Thr Lys Phe Thr  
130 135 140

Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro Leu  
145 150 155 160

Thr Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Asn Asp Asp Gly Leu  
165 170 175



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Glu Glu Leu Val Ser Ala Leu Asn Cys Val Gly Gly Cys Gln Ile Ile  
180 185 190

Val Ser Gln Gly Trp Val Leu Ile Asp Phe Leu Leu Phe Phe Ile Pro  
195 200 205

Thr Leu Val Met Ile Ile Leu Tyr Ser Lys Ile Phe Leu Ile Ala Lys  
210 215 220

Gln Gln Ala Ile Lys Ile Glu Thr Thr Ser Ser Lys Val Glu Ser Ser  
225 230 235 240

Ser Glu Ser Tyr Lys Ile Arg Val Ala Lys Arg Glu Arg Lys Ala Ala  
245 250 255

Lys Thr Leu Gly Val Thr Val Leu Ala Phe Val Ile Ser Trp Leu Pro  
260 265 270

Tyr Thr Val Asp Ile Leu Ile Asp Ala Phe Met Gly Phe Leu Thr Pro  
275 280 285

Ala Tyr Ile Tyr Glu Ile Cys Cys Trp Ser Ala Tyr Tyr Asn Ser Ala  
290 295 300

Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys Ala  
305 310 315 320

Ile Lys Leu Ile Leu Ser Gly Asp Val Leu Lys Ala Ser Ser Ser Thr  
325 330 335

Ile Ser Leu Phe Leu Glu  
340

<210> 15  
<211> 1062  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

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tcggcctgcg gcttgggttt cgtgcccggt gtctactaca gcctcttgct gtgcctcggt 120  
ttaccagcaa atatcttgac agtgatcatc ctctcccagc tgggtggcaag aagacagaag 180  
tcctcctaca actatctctt ggcactcgct gctgccgaca tcttggtcct ctttttcata 240

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gtgtttgtgg acttcctgtt ggaagatttc atcttgaaca tgcagatgcc tcagggtcccc 300  
gacaagatca tagaagtgtct ggaatttctca tccatccaca cctccatattg gattactgtta 360  
ccgttaacca ttgacaggta tatcgtgttc tgccacccgc tcaagtacca cacgggtctca 420  
taccagccc gcacccggaa agtcattgtta agtgtttaca tcacctgctt cctgaccagc 480  
atcccctatt actggtggcc caacatctgg actgaagact acatcagcac ctctgtgcat 540  
cacgtcctca tctggatcca ctgcttcacc gtctacctgg tgccctgctc catcttcttc 600  
atcttgaact caatcattgt gtacaagctc aggaggaaga gcaattttcg tctccgtggc 660  
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tgggcccccc gcatcatcat gattctttac cacctctatg gggcgcccat ccagaaccgc 780  
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aacttcttcc tctactgctt catcagcaag cggttccgca ccatggcagc cgccacgctc 900  
aaggctttct tcaagtgcc gaagcaacct gtacagttct acaccaatca taacttttcc 960  
ataacaagta gcccctggat ctgcccggca aactcacact gcatcaagat gctggtgtac 1020  
cagtatgaca aaaatggaaa acctataaaa gtatccccgt ga 1062

<210> 16  
<211> 353  
<212> PRT  
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<220>  
<223> Sequence

<400> 16

Met Glu His Thr His Ala His Leu Ala Ala Asn Ser Ser Leu Ser Trp  
1 5 10 15

Trp Ser Pro Gly Ser Ala Cys Gly Leu Gly Phe Val Pro Val Val Tyr  
20 25 30

Tyr Ser Leu Leu Leu Cys Leu Gly Leu Pro Ala Asn Ile Leu Thr Val  
35 40 45

Ile Ile Leu Ser Gln Leu Val Ala Arg Arg Gln Lys Ser Ser Tyr Asn  
50 55 60

Tyr Leu Leu Ala Leu Ala Ala Asp Ile Leu Val Leu Phe Phe Ile  
65 70 75 80

Val Phe Val Asp Phe Leu Leu Glu Asp Phe Ile Leu Asn Met Gln Met  
85 90 95

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Pro Gln Val Pro Asp Lys Ile Ile Glu Val Leu Glu Phe Ser Ser Ile  
100 105 110

His Thr Ser Ile Trp Ile Thr Val Pro Leu Thr Ile Asp Arg Tyr Ile  
115 120 125

Ala Val Cys His Pro Leu Lys Tyr His Thr Val Ser Tyr Pro Ala Arg  
130 135 140

Thr Arg Lys Val Ile Val Ser Val Tyr Ile Thr Cys Phe Leu Thr Ser  
145 150 155 160

Ile Pro Tyr Tyr Trp Trp Pro Asn Ile Trp Thr Glu Asp Tyr Ile Ser  
165 170 175

Thr Ser Val His His Val Leu Ile Trp Ile His Cys Phe Thr Val Tyr  
180 185 190

Leu Val Pro Cys Ser Ile Phe Phe Ile Leu Asn Ser Ile Ile Val Tyr  
195 200 205

Lys Leu Arg Arg Lys Ser Asn Phe Arg Leu Arg Gly Tyr Ser Thr Gly  
210 215 220

Lys Thr Thr Ala Ile Leu Phe Thr Ile Thr Ser Ile Phe Ala Thr Leu  
225 230 235 240

Trp Ala Pro Arg Ile Ile Met Ile Leu Tyr His Leu Tyr Gly Ala Pro  
245 250 255

Ile Gln Asn Arg Trp Leu Val His Ile Met Ser Asp Ile Ala Asn Met  
260 265 270

Leu Ala Leu Leu Asn Thr Ala Ile Asn Phe Phe Leu Tyr Cys Phe Ile  
275 280 285

Ser Lys Arg Phe Arg Thr Met Ala Ala Ala Thr Leu Lys Ala Phe Phe  
290 295 300

Lys Cys Gln Lys Gln Pro Val Gln Phe Tyr Thr Asn His Asn Phe Ser  
305 310 315 320

Ile Thr Ser Ser Pro Trp Ile Ser Pro Ala Asn Ser His Cys Ile Lys  
325 330 335

Met Leu Val Tyr Gln Tyr Asp Lys Asn Gly Lys Pro Ile Lys Val Ser  
340 345 350

Pro

<210> 17  
 <211> 969  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

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 ggactgacag gaaacgcggt agtgctctgg ctccctgggct accgcatgcg caggaacgct 180  
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 gtgatgacct ttccctactt tacaggcctg agtatgctga gcgccatcag caccgagcgc 360  
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<210> 18  
 <211> 322  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 18

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 1 5 10 15

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Gly Arg Glu Glu Thr Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val  
20 25 30

Leu Thr Cys Ile Ile Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val  
35 40 45

Leu Trp Leu Leu Gly Tyr Arg Met Arg Arg Asn Ala Val Ser Ile Tyr  
50 55 60

Ile Leu Asn Leu Ala Ala Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile  
65 70 75 80

Ile Arg Ser Pro Leu Arg Leu Ile Asn Ile Ser His Leu Ile Arg Lys  
85 90 95

Ile Leu Val Ser Val Met Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met  
100 105 110

Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile  
115 120 125

Trp Tyr Arg Cys Arg Arg Pro Thr His Leu Ser Ala Val Val Cys Val  
130 135 140

Leu Leu Trp Gly Leu Ser Leu Leu Phe Ser Met Leu Glu Trp Arg Phe  
145 150 155 160

Cys Asp Phe Leu Phe Ser Gly Ala Asp Ser Ser Trp Cys Glu Thr Ser  
165 170 175

Asp Phe Ile Pro Val Ala Trp Leu Ile Phe Leu Cys Val Val Leu Cys  
180 185 190

Val Ser Ser Leu Val Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Lys  
195 200 205

Met Pro Leu Thr Arg Leu Tyr Val Thr Ile Leu Leu Thr Val Leu Val  
210 215 220

Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile Leu Gly Ala Leu Ile Tyr  
225 230 235 240

Arg Met His Leu Asn Leu Glu Val Leu Tyr Cys His Val Tyr Leu Val  
245 250 255

Cys Met Ser Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr  
260 265 270

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Phe Phe Val Gly Ser Phe Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys  
275 280 285

Leu Val Leu Gln Arg Ala Leu Gln Asp Lys Pro Glu Val Asp Lys Gly  
290 295 300

Glu Gly Gln Leu Pro Glu Glu Ser Leu Glu Leu Ser Gly Ser Arg Leu  
305 310 315 320

Gly Pro

<210> 19  
<211> 969  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

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gcgctgacag gaaacgcggt tgtgctctgg ctccctgggct gccgcatgcg caggaacgct 180  
gtctccatct acatcctcaa cctggtcgcg gccgacttcc tcttccttag cggccacatt 240  
atatgttcgc cgttacgcct catcaatatc cgccatccca tctccaaaat cctcagtcct 300  
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aggattctct gtggatcccg gaagatgccg ctgaccaggc tgtacgtgac catcctcctc 660  
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tccgctctta acagcagtgc caaccccatc atttacttct tcgtgggctc ctttaggcag 840  
cgtcaaaata ggcagaacct gaagctgggt ctccagaggg ctctgcagga cagcctgag 900  
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<211> 322

21.US18.CIP.revised.ST25

<212> PRT  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 20

Met Asp Ser Thr Ile Pro Val Leu Gly Thr Glu Leu Thr Pro Ile Asn  
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Gly Arg Glu Glu Thr Pro Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly  
20 25 30

Leu Thr Cys Ile Val Ser Leu Val Ala Leu Thr Gly Asn Ala Val Val  
35 40 45

Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Val Ser Ile Tyr  
50 55 60

Ile Leu Asn Leu Val Ala Ala Asp Phe Leu Phe Leu Ser Gly His Ile  
65 70 75 80

Ile Cys Ser Pro Leu Arg Leu Ile Asn Ile Arg His Pro Ile Ser Lys  
85 90 95

Ile Leu Ser Pro Val Met Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met  
100 105 110

Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Ile Leu Trp Pro Ile  
115 120 125

Trp Tyr His Cys Arg Arg Pro Arg Tyr Leu Ser Ser Val Met Cys Val  
130 135 140

Leu Leu Trp Ala Leu Ser Leu Leu Arg Ser Ile Leu Glu Trp Met Phe  
145 150 155 160

Cys Asp Phe Leu Phe Ser Gly Ala Asp Ser Val Trp Cys Glu Thr Ser  
165 170 175

Asp Phe Ile Thr Ile Ala Trp Leu Val Phe Leu Cys Val Val Leu Cys  
180 185 190

Gly Ser Ser Leu Val Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Lys  
195 200 205

Met Pro Leu Thr Arg Leu Tyr Val Thr Ile Leu Leu Thr Val Leu Val  
210 215 220

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Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Ala Leu Phe Ser  
225 230 235 240

Arg Ile His Leu Asp Trp Lys Val Leu Phe Cys His Val His Leu Val  
245 250 255

Ser Ile Phe Leu Ser Ala Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr  
260 265 270

Phe Phe Val Gly Ser Phe Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys  
275 280 285

Leu Val Leu Gln Arg Ala Leu Gln Asp Thr Pro Glu Val Asp Glu Gly  
290 295 300

Gly Gly Trp Leu Pro Gln Glu Thr Leu Glu Leu Ser Gly Ser Arg Leu  
305 310 315 320

Glu Gln

<210> 21  
<211> 26  
<212> DNA  
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<220>  
<223> Novel Sequence

<400> 21  
cagagctctg gtggccacct ctgtcc

26

<210> 22  
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<212> DNA  
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<220>  
<223> Novel Sequence

<400> 22  
ctgcgtccac cagagtcacg tctcc

25

<210> 23  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 23  
gtatgcctgg ccacaatacc tccagg

26



<210> 24  
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 <400> 24  
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 <210> 25  
 <211> 28  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Novel Sequence  
  
 <400> 25  
 ggtaccacaa tgacaatcac cagcgtcc 28  
  
 <210> 26  
 <211> 29  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Novel Sequence  
  
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 <210> 27  
 <211> 27  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Novel Sequence  
  
 <400> 27  
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 <210> 28  
 <211> 32  
 <212> DNA  
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 <400> 28  
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 <210> 29

<211> 25  
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 gaggtacagc tggcgatgct gacag 25

<210> 30  
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 <212> DNA  
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 <400> 30  
 gtggccatga gccaccctga gctcc 25

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 <400> 31  
 ggaatgtcca ctgaatgcgc gcgg 24

<210> 32  
 <211> 25  
 <212> DNA  
 <213> Artificial  
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 <223> Novel Sequence  
 <400> 32  
 agctcgccag gtgtgagaaa ctcgg 25

<210> 33  
 <211> 30  
 <212> DNA  
 <213> Artificial  
 <220>  
 <223> Novel Sequence  
 <400> 33  
 gcgttatgag cagcaattca tccctgctgg 30

<210> 34  
 <211> 28  
 <212> DNA  
 <213> Artificial

21.US18.CIP.revised.ST25

<220>  
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 <400> 34  
 gtatcctgaa cttcgtctat acaactgc 28  
  
 <210> 35  
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 <400> 35  
 ccctcaggaa tgatgccctt ttgccacaa 29  
  
 <210> 36  
 <211> 28  
 <212> DNA  
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 <223> Novel Sequence  
  
 <400> 36  
 atccatgtgg ttggtgcatg tggttcgt 28  
  
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 <212> DNA  
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 <400> 37  
 aaacaacaaa cagcagaacc atgaccagc 29  
  
 <210> 38  
 <211> 30  
 <212> DNA  
 <213> Artificial  
  
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 <400> 38  
 acatagagac aagtgacatg tgtgaaccac 30  
  
 <210> 39  
 <211> 26  
 <212> DNA  
 <213> Artificial  
  
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 <223> Novel Sequence

<400> 39  
ggtatgagac cgtgtggtac ttgagc 26

<210> 40  
<211> 29  
<212> DNA  
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<220>  
<223> Novel Sequence

<400> 40  
gtggcagaca gcgatatacc tgtcaatgg 29

<210> 41  
<211> 27  
<212> DNA  
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<220>  
<223> Novel Sequence

<400> 41  
gcgctcatgg agcacacgca cgccac 27

<210> 42  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 42  
gaggcagtag ttgccacacc tatgg 25

<210> 43  
<211> 29  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 43  
catctggttt gtgttcccag gggcaccag 29

<210> 44  
<211> 32  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 44  
gacagtgttg ctctcaaagt cccgtctgac tg 32

<210> 45  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 45  
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25

<210> 46  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 46  
 gcagcattgc tctcaaagtc ctgtctg

27

<210> 47  
 <211> 6  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 47

Thr Leu Glu Ser Ile Met  
 1 5

<210> 48  
 <211> 5  
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